

OIPE

RAW SEQUENCE LISTING

DATE: 01/11/2002

PATENT APPLICATION: US/10/024,599

TIME: 12:35:41

Input Set : A:\278-rev.txt

Output Set: N:\CRF3\01112002\J024599.raw

ENTERED

3 <110> APPLICANT: Myriad Genetics, Inc.
 4 Cimbora, Daniel M.
 5 Heichman, Karen
 6 Bartel, Paul L.
 8 <120> TITLE OF INVENTION: Protein-Protein Interactions
 10 <130> FILE REFERENCE: 2318-278-II
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/024,599
 C--> 12 <141> CURRENT FILING DATE: 2001-12-21
 12 <150> PRIOR APPLICATION NUMBER: US 60/256,986
 13 <151> PRIOR FILING DATE: 2000-12-21
 15 <160> NUMBER OF SEQ ID NOS: 6
 17 <170> SOFTWARE: PatentIn version 3.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 40
 21 <212> TYPE: DNA
 C--> 22 <213> ORGANISM: Artificial
 24 <220> FEATURE:
 25 <223> OTHER INFORMATION: oligonucleotide primer
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 31 <211> LENGTH: 39
 32 <212> TYPE: DNA
 C--> 33 <213> ORGANISM: Artificial
 35 <220> FEATURE:
 36 <223> OTHER INFORMATION: oligonucleotide primer
 38 <400> SEQUENCE: 2
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 41 <210> SEQ ID NO: 3
 42 <211> LENGTH: 528
 43 <212> TYPE: DNA
 44 <213> ORGANISM: Homo sapiens
 46 <220> FEATURE:
 47 <221> NAME/KEY: CDS
 48 <222> LOCATION: (1)..(528)
 49 <223> OTHER INFORMATION: Xaa is Gly or Cys
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 53 Ala Asn Arg Asn Gly Gly Tyr Gly Cys Val Cys Val Asn Gly Trp Ser
 54 1 5 10 15
 56 gga gat gac tgc agt gag aac att. gat gat tgt gcc ttc gcc tcc tgt 96
 57 Gly Asp Asp Cys Ser Glu Asn Ile Asp Asp Cys Ala Phe Ala Ser Cys
 58 20 25 30
 60 act cca ggc tcc acc tgc atc gac cgt gtg gcc tcc ttc tct tgc atg 144
 61 Thr Pro Gly Ser Thr Cys Ile Asp Arg Val Ala Ser Phe Ser Cys Met
 62 35 40 45
 64 ttc cca gag ggg aag gca ggt ctc ctg tgt cat ctg gat gat gca tgc 192

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65 Phe Pro Glu Gly Lys Ala Gly Leu Leu Cys His Leu Asp Asp Ala Cys
66      50                      55                      60
68 atc agc aat cct tgc cac aag ggg gca ttg tgt gac acc aac ccc cta      240
69 Ile Ser Asn Pro Cys His Lys Gly Ala Leu Cys Asp Thr Asn Pro Leu
70 65                      70                      75                      80
72 aat ggg caa tat att tgc acc tgc cca caa ggc tac aaa ggg gct gac      288
73 Asn Gly Gln Tyr Ile Cys Thr Cys Pro Gln Gly Tyr Lys Gly Ala Asp
74                      85                      90                      95
76 tgc aca gaa gat gtg gat gaa tgt gcc atg gcc aat agc aat cct tgt      336
77 Cys Thr Glu Asp Val Asp Glu Cys Ala Met Ala Asn Ser Asn Pro Cys
78                      100                      105                      110
80 gag cat gca gga aaa tgt gtg aac acg gat ggc gcc ttc cac tgt gag      384
81 Glu His Ala Gly Lys Cys Val Asn Thr Asp Gly Ala Phe His Cys Glu
82                      115                      120                      125
84 tgt ctg aag ggt tat gca gga cct cgt tgt gag atg gac atc aat gag      432
85 Cys Leu Lys Gly Tyr Ala Gly Pro Arg Cys Glu Met Asp Ile Asn Glu
86                      130                      135                      140
88 tgc cat tca gac ccc tgc cag aat gat gct acc tgt ctg gat aag att      480
89 Cys His Ser Asp Pro Cys Gln Asn Asp Ala Thr Cys Leu Asp Lys Ile
90 145                      150                      155                      160
92 gga ggc ttc aca tgt ctg tgc cat gcc agg ttt caa agg kgt gca ttg      528
W--> 93 Gly Gly Phe Thr Cys Leu Cys His Ala Arg Phe Gln Arg Xaa Ala Leu
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96 <210> SEQ ID NO: 4
97 <211> LENGTH: 176
98 <212> TYPE: PRT
99 <213> ORGANISM: Homo sapiens
101 <220> FEATURE:
102 <221> NAME/KEY: PEPTIDE
103 <222> LOCATION: 1..176
104 <223> OTHER INFORMATION: Xaa is Gly or Cys
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110 Gly Asp Asp Cys Ser Glu Asn Ile Asp Asp Cys Ala Phe Ala Ser Cys
111                      20                      25                      30
113 Thr Pro Gly Ser Thr Cys Ile Asp Arg Val Ala Ser Phe Ser Cys Met
114                      35                      40                      45
116 Phe Pro Glu Gly Lys Ala Gly Leu Leu Cys His Leu Asp Asp Ala Cys
117 50                      55                      60
119 Ile Ser Asn Pro Cys His Lys Gly Ala Leu Cys Asp Thr Asn Pro Leu
120 65                      70                      75                      80
122 Asn Gly Gln Tyr Ile Cys Thr Cys Pro Gln Gly Tyr Lys Gly Ala Asp
123                      85                      90                      95
125 Cys Thr Glu Asp Val Asp Glu Cys Ala Met Ala Asn Ser Asn Pro Cys
126                      100                      105                      110
128 Glu His Ala Gly Lys Cys Val Asn Thr Asp Gly Ala Phe His Cys Glu
129                      115                      120                      125
131 Cys Leu Lys Gly Tyr Ala Gly Pro Arg Cys Glu Met Asp Ile Asn Glu

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132      130      135      140
134 Cys His Ser Asp Pro Cys Gln Asn Asp Ala Thr Cys Leu Asp Lys Ile
135 145      150      155      160
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140 <210> SEQ ID NO: 5
141 <211> LENGTH: 654
142 <212> TYPE: DNA
143 <213> ORGANISM: Homo sapiens
145 <220> FEATURE:
146 <221> NAME/KEY: CDS
147 <222> LOCATION: (1)..(654)
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151 Gln His Arg Asp Pro Cys Glu Lys Asn Arg Cys Gln Asn Gly Gly Thr
152 1      5      10      15
154 tgt gtg gcc cag gcc atg ctg gga aaa gcc acg tgc cgg tgt gcc tca      96
155 Cys Val Ala Gln Ala Met Leu Gly Lys Ala Thr Cys Arg Cys Ala Ser
156      20      25      30
158 ggg ttt aca gga gag gac tgc cag tac tcg aca cct cat cca tgc ttt      144
159 Gly Phe Thr Gly Glu Asp Cys Gln Tyr Ser Thr Pro His Pro Cys Phe
160      35      40      45
162 gtg tct cga cct tgc ctg aat ggc ggc aca tgc cat atg ctc agc cgg      192
163 Val Ser Arg Pro Cys Leu Asn Gly Gly Thr Cys His Met Leu Ser Arg
164 50      55      60
166 gat acc tat gag tgc acc tgt caa gtc ggg ttt aca ggt aag gag tgc      240
167 Asp Thr Tyr Glu Cys Thr Cys Gln Val Gly Phe Thr Gly Lys Glu Cys
168 65      70      75      80
170 caa tgg acc gat gcc tgc ctg tct cat ctc tgt gca aat gga agt acc      288
171 Gln Trp Thr Asp Ala Cys Leu Ser His Leu Cys Ala Asn Gly Ser Thr
172      85      90      95
174 tgt acc act gtg gcc aac cag ttc tcc tgc aaa tgc ctc aca ggc ttc      336
175 Cys Thr Thr Val Ala Asn Gln Phe Ser Cys Lys Cys Leu Thr Gly Phe
176      100      105      110
178 aca ggg cag aag tgt gag act gat gtc aat gag tgt gac att cca gga      384
179 Thr Gly Gln Lys Cys Glu Thr Asp Val Asn Glu Cys Asp Ile Pro Gly
180      115      120      125
182 cac tgc cag ctt ggt ggc acc tgc ctc aac ctg cct ggt tcc tac cag      432
183 His Cys Gln Leu Gly Gly Thr Cys Leu Asn Leu Pro Gly Ser Tyr Gln
184      130      135      140
186 tgc cag tgc ctt cag ggc ttc aca ggc cag tac tgt gac aga ctg tat      480
187 Cys Gln Cys Leu Gln Gly Phe Thr Gly Gln Tyr Cys Asp Arg Leu Tyr
188 145      150      155      160
190 gtg ccc tgt gca cac tcg cct tgt gtc aat gga ggc tcc tgt cgg cag      528
191 Val Pro Cys Ala His Ser Pro Cys Val Asn Gly Gly Ser Cys Arg Gln
192      165      170      175
194 act ggt gac ttc act ttt gag tgc aac tgc ctt cca gag tat gaa gag      576
195 Thr Gly Asp Phe Thr Phe Glu Cys Asn Cys Leu Pro Glu Tyr Glu Glu
196      180      185      190

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198 tgt aag gac ctc ata aaa ttt atg ctg agg aat gag cga cag ttc aag      624
199 Cys Lys Asp Leu Ile Lys Phe Met Leu Arg Asn Glu Arg Gln Phe Lys
200      195      200      205
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203 Glu Glu Phe Leu Phe Ser Ser Leu His Tyr
204      210      215
206 <210> SEQ ID NO: 6
207 <211> LENGTH: 218
208 <212> TYPE: PRT
209 <213> ORGANISM: Homo sapiens
211 <400> SEQUENCE: 6
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213 1      5      10      15
215 Cys Val Ala Gln Ala Met Leu Gly Lys Ala Thr Cys Arg Cys Ala Ser
216      20      25      30
218 Gly Phe Thr Gly Glu Asp Cys Gln Tyr Ser Thr Pro His Pro Cys Phe
219      35      40      45
221 Val Ser Arg Pro Cys Leu Asn Gly Gly Thr Cys His Met Leu Ser Arg
222      50      55      60
224 Asp Thr Tyr Glu Cys Thr Cys Gln Val Gly Phe Thr Gly Lys Glu Cys
225 65      70      75      80
227 Gln Trp Thr Asp Ala Cys Leu Ser His Leu Cys Ala Asn Gly Ser Thr
228      85      90      95
230 Cys Thr Thr Val Ala Asn Gln Phe Ser Cys Lys Cys Leu Thr Gly Phe
231      100      105      110
233 Thr Gly Gln Lys Cys Glu Thr Asp Val Asn Glu Cys Asp Ile Pro Gly
234      115      120      125
236 His Cys Gln Leu Gly Gly Thr Cys Leu Asn Leu Pro Gly Ser Tyr Gln
237      130      135      140
239 Cys Gln Cys Leu Gln Gly Phe Thr Gly Gln Tyr Cys Asp Arg Leu Tyr
240 145      150      155      160
242 Val Pro Cys Ala His Ser Pro Cys Val Asn Gly Gly Ser Cys Arg Gln
243      165      170      175
245 Thr Gly Asp Phe Thr Phe Glu Cys Asn Cys Leu Pro Glu Tyr Glu Glu
246      180      185      190
248 Cys Lys Asp Leu Ile Lys Phe Met Leu Arg Asn Glu Arg Gln Phe Lys
249      195      200      205
251 Glu Glu Phe Leu Phe Ser Ser Leu His Tyr
252      210      215

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VERIFICATION SUMMARY

DATE: 01/11/2002

PATENT APPLICATION: US/10/024,599

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Input Set : A:\278-rev.txt

Output Set: N:\CRF3\01112002\J024599.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:22 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:33 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:93 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:137 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4